

# SEQUENCE LISTING

<110> Prof. Dr. Axel R. Zander

<120> Use of CD34 or a Polypeptide derived therefrom as  
Cell Surface/Gene Transfer Marker

<130> 35-204

<140>

<141>

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1122

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1122)

<223> CD34 (complete length)

<400> 1

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ggg	ttc	atg	agt	ctt	gac	aac	aac	ggt	act	gct	acc	cca	gag	tta	cct	96
Gly	Phe	Met	Ser	Leu	Asp	Asn	Asn	Gly	Thr	Ala	Thr	Pro	Glu	Leu	Pro	
			20					25					30			

acc	cag	gga	aca	ttt	tca	aat	gtt	tct	aca	aat	gta	tcc	tac	caa	gaa	144
Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu	
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act	aca	aca	cct	agt	acc	ctt	gga	agt	acc	agc	ctg	cac	cct	gtg	tct	192
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser	
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caa	cat	ggc	aat	gag	gcc	aca	aca	aac	atc	aca	gaa	acg	aca	gtc	aaa	240
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys	
65					70				75						80	

ttc	aca	tct	acc	tct	gtg	ata	acc	tca	gtt	tat	gga	aac	aca	aac	tct	288
Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser	
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tct	gtc	cag	tca	cag	acc	tct	gta	atc	agc	aca	gtg	ttc	acc	acc	cca	336
Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro	

PatentIn Ver. 2.0

100					105					110							
gcc Ala	aac Asn	gtt Val	tca Ser	act Thr	cca Pro	gag Glu	aca Thr	acc Thr	ttg Leu	aag Lys	cct Pro	agc Ser	ctg Leu	tca Ser	cct Pro	384	
115					120					125							
gga Gly	aat Asn	gtt Val	tca Ser	gac Asp	ctt Leu	tca Ser	acc Thr	act Thr	agc Ser	act Thr	agc Ser	ctt Leu	gca Ala	aca Thr	tct Ser	432	
130					135					140							
ccc Pro	act Thr	aaa Lys	ccc Pro	tat Tyr	aca Thr	tca Ser	tct Ser	tct Ser	cct Pro	atc Ile	cta Leu	agt Ser	gac Asp	atc Ile	aag Lys	480	
145					150					155					160		
gca Ala	gaa Glu	atc Ile	aaa Lys	tgt Cys	tca Ser	ggc Gly	atc Ile	aga Arg	gaa Glu	gtg Val	aaa Lys	ttg Leu	act Thr	cag Gln	ggc Gly	528	
165					170					175							
atc Ile	tgc Cys	ctg Leu	gag Glu	caa Gln	aat Asn	aag Lys	acc Thr	tcc Ser	agc Ser	tgt Cys	gcg Ala	gag Glu	ttt Phe	aag Lys	aag Lys	576	
180					185					190							
gac Asp	agg Arg	gga Gly	gag Glu	ggc Gly	ctg Leu	gcc Ala	cga Arg	gtg Val	ctg Leu	tgt Cys	ggg Gly	gag Glu	gag Glu	cag Gln	gct Ala	624	
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245					250					255							
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275					280					285							
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325					330					335							





gcc aac gtt tca act cca gag aca acc ttg aag cct agc ctg tca cct	384
Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro	
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gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct	432
Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser	
130 135 140	
ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag	480
Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys	
145 150 155 160	
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Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly	
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Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys	
180 185 190	
gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct	624
Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala	
195 200 205	
gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct	672
Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser	
210 215 220	
gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
225 230 235 240	
att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
245 250 255	
aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag	816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
260 265 270	
agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg	864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc	912
Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser	
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 <213> Homo sapiens

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 Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu  
 35 40 45  
 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser  
 50 55 60  
 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys  
 65 70 75 80  
 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser  
 85 90 95  
 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro  
 100 105 110  
 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro  
 115 120 125  
 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser  
 130 135 140  
 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys  
 145 150 155 160  
 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly  
 165 170 175  
 Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys  
 180 185 190  
 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala  
 195 200 205  
 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser  
 210 215 220  
 Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu  
 225 230 235 240  
 Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys  
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 Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln  
 260 265 270  
 Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu  
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 <213> Homo sapiens

<220>  
 <221> CDS

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gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct	672
Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser	
210 215 220	
gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
225 230 235 240	
att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
245 250 255	
aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag	816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
260 265 270	
agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg	864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
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Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu
		35					40				45				
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser
		50				55					60				
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys
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Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser
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Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro
			100					105					110		
Ala	Asn	Val	Ser	Thr	Pro	Glu	Thr	Thr	Leu	Lys	Pro	Ser	Leu	Ser	Pro
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Gly	Asn	Val	Ser	Asp	Leu	Ser	Thr	Thr	Ser	Thr	Ser	Leu	Ala	Thr	Ser
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Pro	Thr	Lys	Pro	Tyr	Thr	Ser	Ser	Ser	Pro	Ile	Leu	Ser	Asp	Ile	Lys
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Ile	Cys	Leu	Glu	Gln	Asn	Lys	Thr	Ser	Ser	Cys	Ala	Glu	Phe	Lys	Lys
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Asp	Ala	Asp	Ala	Gly	Ala	Gln	Val	Cys	Ser	Leu	Leu	Leu	Ala	Gln	Ser
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Glu	Val	Arg	Pro	Gln	Cys	Leu	Leu	Leu	Val	Leu	Ala	Asn	Arg	Thr	Glu
225					230					235					240
Ile	Ser	Ser	Lys	Leu	Gln	Leu	Met	Lys	Lys	His	Gln	Ser	Asp	Leu	Lys
			245						250					255	
Lys	Leu	Gly	Ile	Leu	Asp	Phe	Thr	Glu	Gln	Asp	Val	Ala	Ser	His	Gln
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Ser	Tyr	Ser	Gln	Lys	Thr	Leu	Ile	Ala	Leu	Val	Thr	Ser	Gly	Ala	Leu
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•

34

[illegible]